



1

# SEQUENCE LISTING

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<120> METHOD

<130> 674509-2025.1

<140> 10/693,234  
<141> 2003-10-24

<150> 09/722,938  
<151> 2000-11-27

<150> PCT/IB00/01886  
<151> 2000-11-24

<150> GB 9927801.2  
<151> 1999-11-24

<160> 36

<170> PatentIn Ver. 3.2

<210> 1  
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N-terminal amino acid sequence

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1 5 10

<210> 2  
<211> 61  
<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

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actccatggc tactttgcc caaaaggacc caggttacat tggtattgac gtcaacgctg 60  
9 61

<210> 3  
 <211> 107  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 3  
 cgaaatcgat gttggtacca atccatcttc tgttgaaacc ttgcttcacg gatggcaatc 60  
 ttgggtcagg cttgtctgga gtaccagcgt tgacgtcaat aacaatg 107

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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 4  
 gattggtacc aacatcgatt tcgtttacgt cgtttacact ccacaagggtg cttgtactgc 60  
 tttggacaga gctatggaaa agtgttctcc aggtaccgtc agaatc 106

<210> 5  
 <211> 106  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 5  
 ttcaacaaaa ccagtaacgt tgataatagc cttgacacat tcgtcgaaaa cgaagtcttc 60  
 gtaacagtga ccaccagaaa cgattctgac ggtacctgga gaacac 106

<210> 6  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 6  
 atcaacgtta ctggtttggg tgaatctggg tacgacgacg atagagggtta cttcgtctct 60  
 tccggtgaca ccaactgggg ttcttcaag acctgttca gagaccacgg tagagttttg 120

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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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 gacggagtaa caggaaccac ctggcaaac tctaccgtgg tctctgaac 109

<210> 8  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 8  
 tttggccaga ttgcacggtt tgccagtoga ttggttatcc ggtggtgaag ttgtcgtaa 60  
 gccagtcttg accgaagact ctgttcttaa gtacgttcac aaggattcc 109

<210> 9  
 <211> 116  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 9  
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 tgagcccaaa acaactcacc gtcgttacct tcggaatcct tgtgaacgta cttaag 116

<210> 10  
 <211> 118  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 10  
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 <212> DNA  
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 <212> DNA  
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<400> 12  
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 gccgagagag aagttgccc aacagagac tatcat 96

<210> 13  
 <211> 102  
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<400> 13  
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 <211> 90  
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 aggaccggaa ccgttgatag tctcagtcaa agcgtagaaa gggtagtcca tagtctcgtc 120

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 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Synthetic  
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<400> 16  
 gactttccag acttccagat tgatgttatc tggaaatacc ttactgaggt tcttgacggt 60  
 ttgactagtg ccgaaatgaa ggatgctctt cttcagggtg atatgttc 108

<210> 17  
 <211> 126  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 17  
 cttgtcttct tcttgccagt atgtctggta ctgcagtttg atgatgtact ctctctgagc 60  
 aactgcagta gcatcccaaa caaccttggt aatctcacca ccgaacatat caacctgaag 120  
 aagagc 126

<210> 18  
 <211> 108  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 18  
 acatactggc aggaagaaga caaggatgca gttaacttga agtggattag agacttttac 60  
 gaggagatgt atgagcctta tgggtggtgt ccagacccta acactcag 108

<210> 19  
 <211> 111  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 19  
 ggcaccatac ttaccgttct tccagttggt caagtcaaca tcagggtagt tgaagtagca 60  
 tccctcaaaa acacctttac cactctcaac ctgagtgtta gggctctggaa c 111

<210> 20  
 <211> 117  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 20  
 aagaacggta agtatgggtgc cttggaactt tactttttgg gtaacctgaa cagattgatc 60  
 aaggccaaat gggtgtggga tcctaacgag atcttcacaa acaaacagtc tatccct 117

<210> 21  
 <211> 78  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 21  
 gaattccgcg gccgcctact atttagtctg cttaggctcc ttaagagggt tagtagggat 60  
 agactgtttg tttgtgaa 78

<210> 22  
 <211> 1644  
 <212> DNA  
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<220>  
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 sequence of synthetic Hox gene

<220>  
 <221> CDS  
 <222> (1)..(1644)

&lt;400&gt; 22

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| atg gct act ttg cca caa aag gac cca ggt tac att gtt att gac gtc | 48  |
| Met Ala Thr Leu Pro Gln Lys Asp Pro Gly Tyr Ile Val Ile Asp Val |     |
| 1 5 10 15   |     |
| aac gct ggt act cca gac aag cct gac cca aga ttg cca tcc atg aag | 96  |
| Asn Ala Gly Thr Pro Asp Lys Pro Asp Pro Arg Leu Pro Ser Met Lys |     |
| 20 25 30  |     |
| caa ggt ttc aac aga aga tgg att ggt acc aac atc gat ttc gtt tac | 144 |
| Gln Gly Phe Asn Arg Arg Trp Ile Gly Thr Asn Ile Asp Phe Val Tyr |     |
| 35 40 45  |     |
| gtc gtt tac act cca caa ggt gct tgt act gct ttg gac aga gct atg | 192 |
| Val Val Tyr Thr Pro Gln Gly Ala Cys Thr Ala Leu Asp Arg Ala Met |     |
| 50 55 60  |     |
| gaa aag tgt tct cca ggt acc gtc aga atc gtt tct ggt ggt cac tgt | 240 |
| Glu Lys Cys Ser Pro Gly Thr Val Arg Ile Val Ser Gly Gly His Cys |     |
| 65 70 75 80   |     |
| tac gaa gac ttc gtt ttc gac gaa tgt gtc aag gct att atc aac gtt | 288 |
| Tyr Glu Asp Phe Val Phe Asp Glu Cys Val Lys Ala Ile Ile Asn Val |     |
| 85 90 95  |     |
| act ggt ttg gtt gaa tct ggt tac gac gac gat aga ggt tac ttc gtc | 336 |
| Thr Gly Leu Val Glu Ser Gly Tyr Asp Asp Asp Arg Gly Tyr Phe Val |     |
| 100 105 110   |     |
| tct tcc ggt gac acc aac tgg ggt tcc ttc aag acc ttg ttc aga gac | 384 |
| Ser Ser Gly Asp Thr Asn Trp Gly Ser Phe Lys Thr Leu Phe Arg Asp |     |
| 115 120 125   |     |
| cac ggt aga gtt ttg cca ggt ggt tcc tgt tac tcc gtc ggt ttg ggt | 432 |
| His Gly Arg Val Leu Pro Gly Gly Ser Cys Tyr Ser Val Gly Leu Gly |     |
| 130 135 140   |     |
| ggt cac att gtc ggt gga ggt gac ggt att ttg gcc aga ttg cac ggt | 480 |
| Gly His Ile Val Gly Gly Gly Asp Gly Ile Leu Ala Arg Leu His Gly |     |
| 145 150 155 160   |     |
| ttg cca gtc gat tgg tta tcc ggt gtt gaa gtt gtc gtt aag cca gtc | 528 |
| Leu Pro Val Asp Trp Leu Ser Gly Val Glu Val Val Val Lys Pro Val |     |
| 165 170 175   |     |
| ttg acc gaa gac tct gtt ctt aag tac gtt cac aag gat tcc gaa ggt | 576 |
| Leu Thr Glu Asp Ser Val Leu Lys Tyr Val His Lys Asp Ser Glu Gly |     |
| 180 185 190   |     |
| aac gac ggt gag ttg ttt tgg gct cac act ggt gga ggt gga ggt aac | 624 |
| Asn Asp Gly Glu Leu Phe Trp Ala His Thr Gly Gly Gly Gly Gly Asn |     |
| 195 200 205   |     |
| ttc ggt att atc acc aaa tac tac ttc aag gat ttg cca atg tct cca | 672 |
| Phe Gly Ile Ile Thr Lys Tyr Tyr Phe Lys Asp Leu Pro Met Ser Pro |     |
| 210 215 220   |     |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| aga<br>Arg<br>225 | ggg<br>Gly        | gtc<br>Val        | atc<br>Ile        | gct<br>Ala        | tct<br>Ser<br>230 | aac<br>Asn        | tta<br>Leu        | cac<br>His        | ttc<br>Phe        | tct<br>Ser<br>235 | tgg<br>Trp        | gac<br>Asp        | ggg<br>Gly        | ttc<br>Phe        | act<br>Thr<br>240 | 720  |
| aga<br>Arg        | gat<br>Asp        | gcc<br>Ala        | ttg<br>Leu        | caa<br>Gln<br>245 | gat<br>Asp        | ttg<br>Leu        | ttg<br>Leu        | act<br>Thr        | aag<br>Lys<br>250 | tac<br>Tyr        | ttc<br>Phe        | aag<br>Lys        | ttg<br>Leu        | gct<br>Ala<br>255 | aga<br>Arg        | 768  |
| tgt<br>Cys        | gat<br>Asp        | tgg<br>Trp        | aag<br>Lys<br>260 | aat<br>Asn        | act<br>Thr        | gtt<br>Val        | ggg<br>Gly        | aag<br>Lys<br>265 | ttc<br>Phe        | caa<br>Gln        | atc<br>Ile        | ttc<br>Phe        | cac<br>His<br>270 | caa<br>Gln        | gca<br>Ala        | 816  |
| gct<br>Ala        | gaa<br>Glu        | gag<br>Glu<br>275 | ttt<br>Phe        | gtt<br>Val        | atg<br>Met        | tac<br>Tyr        | ttg<br>Leu<br>280 | tat<br>Tyr        | aca<br>Thr        | tcc<br>Ser        | tac<br>Tyr        | tct<br>Ser<br>285 | aac<br>Asn        | gac<br>Asp        | gcc<br>Ala        | 864  |
| gag<br>Glu<br>290 | aga<br>Arg        | gaa<br>Glu        | gtt<br>Val        | gcc<br>Ala        | caa<br>Gln<br>295 | gac<br>Asp        | aga<br>Arg        | cac<br>His        | tat<br>Tyr        | cat<br>His<br>300 | ttg<br>Leu        | gag<br>Glu        | gct<br>Ala        | gac<br>Asp        | att<br>Ile        | 912  |
| gaa<br>Glu<br>305 | cag<br>Gln        | atc<br>Ile        | tac<br>Tyr        | aaa<br>Lys<br>310 | aca<br>Thr        | tgc<br>Cys        | gag<br>Glu        | cct<br>Pro        | acc<br>Thr<br>315 | aaa<br>Lys<br>315 | gct<br>Ala        | ctt<br>Leu        | ggg<br>Gly        | ggg<br>Gly        | cat<br>His<br>320 | 960  |
| gct<br>Ala        | ggg<br>Gly        | tgg<br>Trp        | gct<br>Ala        | cct<br>Pro<br>325 | ttc<br>Phe        | cct<br>Pro        | gtt<br>Val        | aga<br>Arg        | cct<br>Pro<br>330 | aga<br>Arg        | aag<br>Lys        | aga<br>Arg        | cac<br>His        | aca<br>Thr<br>335 | tcc<br>Ser        | 1008 |
| aag<br>Lys        | act<br>Thr        | tct<br>Ser        | tat<br>Tyr<br>340 | atg<br>Met        | cat<br>His        | gac<br>Asp        | gag<br>Glu        | act<br>Thr<br>345 | atg<br>Met        | gac<br>Asp        | tac<br>Tyr        | cct<br>Pro        | ttc<br>Phe<br>350 | tac<br>Tyr        | gct<br>Ala        | 1056 |
| ttg<br>Leu        | act<br>Thr<br>355 | gag<br>Glu        | act<br>Thr        | atc<br>Ile        | aac<br>Asn        | ggg<br>Gly        | tcc<br>Ser<br>360 | ggg<br>Gly        | cct<br>Pro        | aat<br>Asn        | cag<br>Gln        | aga<br>Arg<br>365 | ggg<br>Gly        | aag<br>Lys        | tac<br>Tyr        | 1104 |
| aag<br>Lys<br>370 | tct<br>Ser        | gct<br>Ala        | tac<br>Tyr        | atg<br>Met        | atc<br>Ile        | aag<br>Lys<br>375 | gac<br>Asp        | ttt<br>Phe        | cca<br>Pro        | gac<br>Asp        | ttc<br>Phe<br>380 | cag<br>Gln        | att<br>Ile        | gat<br>Asp        | gtt<br>Val        | 1152 |
| atc<br>Ile<br>385 | tgg<br>Trp        | aaa<br>Lys        | tac<br>Tyr        | ctt<br>Leu        | act<br>Thr<br>390 | gag<br>Glu        | gtt<br>Val        | cct<br>Pro        | gac<br>Asp        | ggg<br>Gly<br>395 | ttg<br>Leu        | act<br>Thr        | agt<br>Ser        | gcc<br>Ala        | gaa<br>Glu<br>400 | 1200 |
| atg<br>Met        | aag<br>Lys        | gat<br>Asp        | gct<br>Ala        | ctt<br>Leu<br>405 | ctt<br>Leu        | cag<br>Gln        | gtt<br>Val        | gat<br>Asp        | atg<br>Met<br>410 | ttc<br>Phe        | ggg<br>Gly        | ggg<br>Gly        | gag<br>Glu        | att<br>Ile<br>415 | cac<br>His        | 1248 |
| aag<br>Lys        | gtt<br>Val        | gtt<br>Val        | tgg<br>Trp<br>420 | gat<br>Asp        | gct<br>Ala        | act<br>Thr        | gca<br>Ala        | gtt<br>Val<br>425 | gct<br>Ala        | cag<br>Gln        | aga<br>Arg        | gag<br>Glu        | tac<br>Tyr<br>430 | atc<br>Ile        | atc<br>Ile        | 1296 |
| aaa<br>Lys        | ctg<br>Leu        | cag<br>Gln<br>435 | tac<br>Tyr        | cag<br>Gln        | aca<br>Thr        | tac<br>Tyr        | tgg<br>Trp<br>440 | cag<br>Gln        | gaa<br>Glu        | gaa<br>Glu        | gac<br>Asp<br>445 | aag<br>Lys        | gat<br>Asp        | gca<br>Ala        | gtt<br>Val        | 1344 |



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aac ttg aag tgg att aga gac ttt tac gag gag atg tat gag cct tat 1392
Asn Leu Lys Trp Ile Arg Asp Phe Tyr Glu Glu Met Tyr Glu Pro Tyr
450 455 460

ggg ggt gtt cca gac cct aac act cag gtt gag agt ggt aaa ggt gtt 1440
Gly Gly Val Pro Asp Pro Asn Thr Gln Val Glu Ser Gly Lys Gly Val
465 470 475 480

ttt gag gga tgc tac ttc aac tac cct gat gtt gac ttg aac aac tgg 1488
Phe Glu Gly Cys Tyr Phe Asn Tyr Pro Asp Val Asp Leu Asn Asn Trp
485 490 495

aag aac ggt aag tat ggt gcc ttg gaa ctt tac ttt ttg ggt aac ctg 1536
Lys Asn Gly Lys Tyr Gly Ala Leu Glu Leu Tyr Phe Leu Gly Asn Leu
500 505 510

aac aga ttg atc aag gcc aaa tgg ttg tgg gat cct aac gag atc ttc 1584
Asn Arg Leu Ile Lys Ala Lys Trp Leu Trp Asp Pro Asn Glu Ile Phe
515 520 525

aca aac aaa cag tct atc cct act aaa cct ctt aag gag cct aag cag 1632
Thr Asn Lys Gln Ser Ile Pro Thr Lys Pro Leu Lys Glu Pro Lys Gln
530 535 540

act aaa tag tag 1644
Thr Lys
545

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<210> 23
<211> 546
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Amino acid
sequence of synthetic Hox gene

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<400> 23
Met Ala Thr Leu Pro Gln Lys Asp Pro Gly Tyr Ile Val Ile Asp Val
1 5 10 15

Asn Ala Gly Thr Pro Asp Lys Pro Asp Pro Arg Leu Pro Ser Met Lys
20 25 30

Gln Gly Phe Asn Arg Arg Trp Ile Gly Thr Asn Ile Asp Phe Val Tyr
35 40 45

Val Val Tyr Thr Pro Gln Gly Ala Cys Thr Ala Leu Asp Arg Ala Met
50 55 60

Glu Lys Cys Ser Pro Gly Thr Val Arg Ile Val Ser Gly Gly His Cys
65 70 75 80

Tyr Glu Asp Phe Val Phe Asp Glu Cys Val Lys Ala Ile Ile Asn Val
85 90 95

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Thr Gly Leu Val Glu Ser Gly Tyr Asp Asp Asp Arg Gly Tyr Phe Val  
 100 105 110  
 Ser Ser Gly Asp Thr Asn Trp Gly Ser Phe Lys Thr Leu Phe Arg Asp  
 115 120 125  
 His Gly Arg Val Leu Pro Gly Gly Ser Cys Tyr Ser Val Gly Leu Gly  
 130 135 140  
 Gly His Ile Val Gly Gly Gly Asp Gly Ile Leu Ala Arg Leu His Gly  
 145 150 155 160  
 Leu Pro Val Asp Trp Leu Ser Gly Val Glu Val Val Val Lys Pro Val  
 165 170 175  
 Leu Thr Glu Asp Ser Val Leu Lys Tyr Val His Lys Asp Ser Glu Gly  
 180 185 190  
 Asn Asp Gly Glu Leu Phe Trp Ala His Thr Gly Gly Gly Gly Gly Asn  
 195 200 205  
 Phe Gly Ile Ile Thr Lys Tyr Tyr Phe Lys Asp Leu Pro Met Ser Pro  
 210 215 220  
 Arg Gly Val Ile Ala Ser Asn Leu His Phe Ser Trp Asp Gly Phe Thr  
 225 230 235 240  
 Arg Asp Ala Leu Gln Asp Leu Leu Thr Lys Tyr Phe Lys Leu Ala Arg  
 245 250 255  
 Cys Asp Trp Lys Asn Thr Val Gly Lys Phe Gln Ile Phe His Gln Ala  
 260 265 270  
 Ala Glu Glu Phe Val Met Tyr Leu Tyr Thr Ser Tyr Ser Asn Asp Ala  
 275 280 285  
 Glu Arg Glu Val Ala Gln Asp Arg His Tyr His Leu Glu Ala Asp Ile  
 290 295 300  
 Glu Gln Ile Tyr Lys Thr Cys Glu Pro Thr Lys Ala Leu Gly Gly His  
 305 310 315 320  
 Ala Gly Trp Ala Pro Phe Pro Val Arg Pro Arg Lys Arg His Thr Ser  
 325 330 335  
 Lys Thr Ser Tyr Met His Asp Glu Thr Met Asp Tyr Pro Phe Tyr Ala  
 340 345 350  
 Leu Thr Glu Thr Ile Asn Gly Ser Gly Pro Asn Gln Arg Gly Lys Tyr  
 355 360 365  
 Lys Ser Ala Tyr Met Ile Lys Asp Phe Pro Asp Phe Gln Ile Asp Val  
 370 375 380  
 Ile Trp Lys Tyr Leu Thr Glu Val Pro Asp Gly Leu Thr Ser Ala Glu  
 385 390 395 400

Met Lys Asp Ala Leu Leu Gln Val Asp Met Phe Gly Gly Glu Ile His  
                             405                            410                            415  
 Lys Val Val Trp Asp Ala Thr Ala Val Ala Gln Arg Glu Tyr Ile Ile  
                             420                            425                            430  
 Lys Leu Gln Tyr Gln Thr Tyr Trp Gln Glu Glu Asp Lys Asp Ala Val  
                             435                            440                            445  
 Asn Leu Lys Trp Ile Arg Asp Phe Tyr Glu Glu Met Tyr Glu Pro Tyr  
                             450                            455                            460  
 Gly Gly Val Pro Asp Pro Asn Thr Gln Val Glu Ser Gly Lys Gly Val  
                             465                            470                            475                            480  
 Phe Glu Gly Cys Tyr Phe Asn Tyr Pro Asp Val Asp Leu Asn Asn Trp  
                             485                            490                            495  
 Lys Asn Gly Lys Tyr Gly Ala Leu Glu Leu Tyr Phe Leu Gly Asn Leu  
                             500                            505                            510  
 Asn Arg Leu Ile Lys Ala Lys Trp Leu Trp Asp Pro Asn Glu Ile Phe  
                             515                            520                            525  
 Thr Asn Lys Gln Ser Ile Pro Thr Lys Pro Leu Lys Glu Pro Lys Gln  
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 Thr Lys  
 545

<210> 24  
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 <213> Schwanniomyces occidentalis

<400> 24  
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   1                            5

<210> 25  
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 <212> PRT  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
           amino acid signal sequence

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<210> 26  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
 amino acid signal sequence

<400> 26  
 Ala Thr Leu Pro  
 1

<210> 27  
 <211> 6  
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 <213> *Saccharomyces cerevisiae*

<400> 27  
 Lys Arg Glu Ala Glu Ala  
 1 5

<210> 28  
 <211> 5  
 <212> PRT  
 <213> *Aspergillus oryzae*

<400> 28  
 Ala Pro Ala Leu Ala  
 1 5

<210> 29  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 29  
 gaattcatga ccgcattgtc cgacaaacaa acggct

36

<210> 30  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 30  
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<210> 31  
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<220>  
 <223> Description of Artificial Sequence: Synthetic primer

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<210> 32  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<400> 32  
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 <223> Description of Artificial Sequence: Synthetic primer

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<220>  
 <223> Description of Artificial Sequence: Synthetic primer

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<210> 35

<211> 20

<212> PRT

<213> Hansenula polymorpha

<400> 35

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Val Gly Val Trp  
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<210> 36

<211> 31

<212> PRT

<213> Gracilariopsis lemaneiformis

<400> 36

Thr Ala Leu Ser Asp Lys Gln Thr Ala Thr Ala Gly Ser Thr Asp Asn  
 1 5 10 15

Pro Asp Gly Ile Asp Tyr Lys Thr Tyr Asp Tyr Val Gly Val Trp  
 20 25 30